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#14

RAW SEQUENCE LISTING

DATE: 09/08/2003

PATENT APPLICATION: US/09/011,307

TIME: 13:26:27

Input Set : N:\EBONY'S\US09011307.raw.txt

Output Set: N:\CRF4\09082003\I011307.raw

SEQUENCE LISTING

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1 (1) GENERAL INFORMATION:
2   (i) APPLICANT: Zabeau, Marc
3           Vos, Pieter
4           Simons, Guus
5   (ii) TITLE OF INVENTION: RESISTANCE AGAINST WILT INDUCING FUNGI
6   (iii) NUMBER OF SEQUENCES: 12
7   (iv) CORRESPONDENCE ADDRESS:
8       (A) ADDRESSEE: SPENCER & FRANK
9       (B) STREET: 1100 New York Avenue, N.W., Suite 300 East
10      (C) CITY: Washington
11      (D) STATE: DC
12      (E) COUNTRY: USA
13      (F) ZIP: 20005
14   (v) COMPUTER READABLE FORM:
15       (A) MEDIUM TYPE: Floppy disk
16       (B) COMPUTER: IBM PC compatible
17       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
18       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
19   (vi) CURRENT APPLICATION DATA:
C--> 20       (A) APPLICATION NUMBER: US/09/011,307
C--> 21       (B) FILING DATE: 01-Jul-1988
22       (C) CLASSIFICATION:
23   (vii) PRIOR APPLICATION DATA:
24       (A) APPLICATION NUMBER: EP 95401849.5
25       (B) FILING DATE: 07-AUG-1995
26   (viii) ATTORNEY/AGENT INFORMATION:
27       (A) NAME: Gollin, Michael A.
28       (B) REGISTRATION NUMBER: 31,957
29       (C) REFERENCE/DOCKET NUMBER: GUPLA 0008
30   (ix) TELECOMMUNICATION INFORMATION:
31       (A) TELEPHONE: 202-414-4000
32       (B) TELEFAX: 202-414-4040
33 (2) INFORMATION FOR SEQ ID NO: 1:
34   (i) SEQUENCE CHARACTERISTICS:
35       (A) LENGTH: 19 base pairs
36       (B) TYPE: nucleic acid
37       (C) STRANDEDNESS: single
38       (D) TOPOLOGY: linear
39   (ii) MOLECULE TYPE: other nucleic acid
40       (A) DESCRIPTION: /desc = "primer"
41   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
42       GACTGCGTAC CAATTCNNN

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44 (2) INFORMATION FOR SEQ ID NO: 2:
45     (i) SEQUENCE CHARACTERISTICS:
46         (A) LENGTH: 19 base pairs
47         (B) TYPE: nucleic acid
48         (C) STRANDEDNESS: single
49         (D) TOPOLOGY: linear
50     (ii) MOLECULE TYPE: other nucleic acid
51         (A) DESCRIPTION: /desc = "primer"
52     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
53     GATGAGTCCT GAGTAANNN
54
55 (2) INFORMATION FOR SEQ ID NO: 3:
56     (i) SEQUENCE CHARACTERISTICS:
57         (A) LENGTH: 17 base pairs
58         (B) TYPE: nucleic acid
59         (C) STRANDEDNESS: single
60         (D) TOPOLOGY: linear
61     (ii) MOLECULE TYPE: other nucleic acid
62         (A) DESCRIPTION: /desc = "oligonucleotide"
63     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
64     CTCGTAGACT GCGTACC
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66 (2) INFORMATION FOR SEQ ID NO: 4:
67     (i) SEQUENCE CHARACTERISTICS:
68         (A) LENGTH: 18 base pairs
69         (B) TYPE: nucleic acid
70         (C) STRANDEDNESS: single
71         (D) TOPOLOGY: linear
72     (ii) MOLECULE TYPE: other nucleic acid
73         (A) DESCRIPTION: /desc = "oligonucleotide"
74     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
75     AATTGGTACG CAGTCTAC
76
77 (2) INFORMATION FOR SEQ ID NO: 5:
78     (i) SEQUENCE CHARACTERISTICS:
79         (A) LENGTH: 16 base pairs
80         (B) TYPE: nucleic acid
81         (C) STRANDEDNESS: single
82         (D) TOPOLOGY: linear
83     (ii) MOLECULE TYPE: other nucleic acid
84         (A) DESCRIPTION: /desc = "oligonucleotide"
85     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
86     GACGATGAGT CCTGAG
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88 (2) INFORMATION FOR SEQ ID NO: 6:
89     (i) SEQUENCE CHARACTERISTICS:
90         (A) LENGTH: 14 base pairs
91         (B) TYPE: nucleic acid
92         (C) STRANDEDNESS: single
93         (D) TOPOLOGY: linear
94     (ii) MOLECULE TYPE: other nucleic acid
95         (A) DESCRIPTION: /desc = "oligonucleotide"
96     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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97      TACTCAGGAC TCAT
99 (2)  INFORMATION FOR SEQ ID NO: 7:
100      (i) SEQUENCE CHARACTERISTICS:
101          (A) LENGTH: 16 base pairs
102          (B) TYPE: nucleic acid
103          (C) STRANDEDNESS: single
104          (D) TOPOLOGY: linear
105      (ii) MOLECULE TYPE: other nucleic acid
106          (A) DESCRIPTION: /desc = "primer"
107      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
108      GACTGCGTAC CAATTC
110 (2)  INFORMATION FOR SEQ ID NO: 8:
111      (i) SEQUENCE CHARACTERISTICS:
112          (A) LENGTH: 16 base pairs
113          (B) TYPE: nucleic acid
114          (C) STRANDEDNESS: single
115          (D) TOPOLOGY: linear
116      (ii) MOLECULE TYPE: other nucleic acid
117          (A) DESCRIPTION: /desc = "primer"
118      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
119      GATGAGTCCT GAGTAA
121 (2)  INFORMATION FOR SEQ ID NO: 9:
122      (i) SEQUENCE CHARACTERISTICS:
123          (A) LENGTH: 19 base pairs
124          (B) TYPE: nucleic acid
125          (C) STRANDEDNESS: single
126          (D) TOPOLOGY: linear
127      (ii) MOLECULE TYPE: other nucleic acid
128          (A) DESCRIPTION: /desc = "primer"
129      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
130      GACTGCGTAC CAATTCAGA
132 (2)  INFORMATION FOR SEQ ID NO: 10:
133      (i) SEQUENCE CHARACTERISTICS:
134          (A) LENGTH: 19 base pairs
135          (B) TYPE: nucleic acid
136          (C) STRANDEDNESS: single
137          (D) TOPOLOGY: linear
138      (ii) MOLECULE TYPE: other nucleic acid
139          (A) DESCRIPTION: /desc = "primer"
140      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
141      GATGAGTCCT GAGTAATCT
143 (2)  INFORMATION FOR SEQ ID NO: 11:
144      (i) SEQUENCE CHARACTERISTICS:
145          (A) LENGTH: 6658 base pairs
146          (B) TYPE: nucleic acid
147          (C) STRANDEDNESS: single
148          (D) TOPOLOGY: linear
149      (ii) MOLECULE TYPE: cDNA
150      (ix) FEATURE:

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151      (A) NAME/KEY: CDS
152      (B) LOCATION: 1798..5595
153      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
154      AAAAAAGCAG CTTTAAAAAA AGTACTTTKG AAAGGKGCTG AAACCTTATTT TTTGAAATAA      60
155      GCAGTTATGT GTTTGGAAWA AAAGTGCTGA AGTTGCTATG TCAAAACATGA AAAGGGRAAA      120
156      AATGGAAGAA AGAGWTGTTA GGGTTATGTC GTAATTTGGA GATTGTATAA AAATATTAAG      180
157      GGCAAAAAAA ATAAAAATGT GTCAACTTAA AACAGCTTAT AAGCTAAAAAG TTAAAGCTGC      240
158      GGGTAGAGGT GTTTTTTTTT TTTTAGCTT ATAAGTTGTT TTAAGTTGAC CACATTTTTTA      300
159      TTTTTKTTGC CCTTAATATT TTTATACAAT CTCAAAATTA CGACATAACC CTAACATCTT      360
160      TTTTCCCCAT TTTTTCCTTT TCACGTTTGA CATAGCAACT TCAGCACTTT TATCCAAACA      420
161      CATAACTGCT TATTTTAAAA ATAAGTTTCA GCACTTTCAA AAGTACTTTT TTAAAGCTGC      480
162      TTTTATTAAG CCCATCCAAA CGGGCCCTAA AATTGCTAAT GTTTGCTCTT TCTATTCTCA      540
163      AACTCCGTAA TATTTAAGAA AATTTGCTAA TGATAGGTCA CTTTAAACAC TAAATAATTA      600
164      TAAATTGGGT AGAAATTTAT TTATCATTTT AAGCTTTTTT AATTTTGAGT CTTCTCCCTA      660
165      ATTAAGACCC TTCCCTCTT GCTTCAATTA TTTAACTGAA TAGTCTTTGT CTTATTGTTG      720
166      GGTGAAAGTC TGTCTTCTTG TTAGGTAATA AGTCCTACAA TAATATCAAT AATTGCTAT      780
167      GGAGAAAAAA ATATTATAGG AGAAAAATAA TTAATTTTAA TTCATGAATA TGCTTAATA      840
168      TGCAACTCAT TTTGCTTATA TATATCAAAT TAACTCTGT TCCTTTAACT TTTTCCTATG      900
169      AAGATACATT TTAATTTATT TGATGAGGTT AGTTTGGAAA TTTATATTAT AATAATGAAA      960
170      TGATATAACT TAAAAGAAGT TGTTTGATAT CTTATCAGAA TCATGCAGGT ACTCATAATA      1020
171      TAAGAAATAA TTATGATGAA ATTTATATAT GTTTTATGCA GAGATTTATT ACGCATTGTT      1080
172      TACTTGGGTT ATGTATTACT TATTTTCATCT TTTATCAGAA TGTAATAATA TCATTCAATA      1140
173      AGAAATCCAA TTCTGTTAAA TTCAAAATAC AAACAATAAC ATTTTCAAGA CCGATTTTTT      1200
174      GCCCAAGAAT ATACAGTAAA CATATTTATG ATATGGTAGG TCTCTTTAGT AATTGACCAA      1260
175      CAAGGATTGT GGTGGAGTGG GAAATACTCT TTAATACTTC ACCAAGAGGT CTCCAATTTG      1320
176      AGCCCCTGAA TACGAAATCG TCTTTGTTAG TATATACCCT AACCTAATAC AAAAATTAGT      1380
177      ATATTAGCCT TNACAGCTAA AATCTTTGTG ACCTGTAAGT CACGCGAGGA CAAATTTACC      1440
178      GTAAACCAA CTTATTCATG ATATAATTGT CCTTTTAGC ACGGTAATAA TGAGGTGGGT      1500
179      AGAAATTTAT TACTTGAGGG CCCTTCTAC ACCCACCCTT ATTCTCTGC TTCAATTATT      1560
180      GAATTGAAGA AGTAATGAAA AAACAGACTC CATTGGATAA AGGACAGTTT GCAAACACAG      1620
181      CTGTAACAAT TTAGAGCACT AGCAAAATAG AGAGAGTTTT GAGAGAAATT TTTGTTTGCA      1680
182      AATTACTCTT AACCTTCAGC AGGTAAAATA AAGTCTTAA CTGAGACTAT TTGAAGATAT      1740
183      ATTTTGTTAA AGAATCATTT TGTGTGTTTC CTTGTTTTCG TTTTGCAGAT TTGAGAA      1797
184      ATG GAG ATT GGC TTA GCA GTT GGT GGT GCA TTT CTC TCC TCA GCT TTG      1845
185      Met Glu Ile Gly Leu Ala Val Gly Gly Ala Phe Leu Ser Ser Ala Leu
186      1 5 10 15
187      AAT GTT CTG TTT GAT AGG CTT GCT CCT AAC GGT GAT CTG CTC AAC ATG      1893
188      Asn Val Leu Phe Asp Arg Leu Ala Pro Asn Gly Asp Leu Leu Asn Met
189      20 25 30
190      TTT CGG AAG CAT AAG GAT CAT GTT AAG CTC TTA AAG AAG CTG AAA ATG      1941
191      Phe Arg Lys His Lys Asp His Val Lys Leu Leu Lys Lys Leu Lys Met
192      35 40 45
193      ACT TTG CGT GGT ATT CAG ATT GTG CTA AGT GAT GCA GAG AAT AAG CAA      1989
194      Thr Leu Arg Gly Ile Gln Ile Val Leu Ser Asp Ala Glu Asn Lys Gln
195      50 55 60
196      GCA TCA AAT CCA TCT GTG AGA GAC TGG CTT AAT GAG CTT CGA GAT GCT      2037
197      Ala Ser Asn Pro Ser Val Arg Asp Trp Leu Asn Glu Leu Arg Asp Ala
198      65 70 75 80
199      GTC GAC TCT GCT GAA AAT TTA ATA GAA GAA GTC AAT TAT GAA GCT TTG      2085

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200	Val Asp Ser Ala Glu Asn Leu Ile Glu Glu Val Asn Tyr Glu Ala Leu	
201	85 90 95	
202	AGG CTT AAG GTG GAA GGT CAG CAT CAG AAT TTT TCA GAA ACA AGC AAC	2133
203	Arg Leu Lys Val Glu Gly Gln His Gln Asn Phe Ser Glu Thr Ser Asn	
204	100 105 110	
205	CAG CAA GTA AGT GAT GAT TTT TTC CTT AAC ATA AAG GAC AAG CTG GAA	2181
206	Gln Gln Val Ser Asp Asp Phe Phe Leu Asn Ile Lys Asp Lys Leu Glu	
207	115 120 125	
208	GAC ACT ATT GAA ACA TTA AAG GAT TTG CAA GAG CAA ATT GGT CTC CTT	2229
209	Asp Thr Ile Glu Thr Leu Lys Asp Leu Gln Glu Ile Gly Leu Leu	
210	130 135 140	
211	GGC TTA AAG GAG TAT TTT GAT TCC ACG AAA CTA GAA ACT AGA AGA CCT	2277
212	Gly Leu Lys Glu Tyr Phe Asp Ser Thr Lys Leu Glu Thr Arg Arg Pro	
213	145 150 155 160	
214	TCA ACT TCT GTG GAT GAT GAA TCT GAT ATC TTT GGT AGG CAG AGC GAA	2325
215	Ser Thr Ser Val Asp Asp Glu Ser Asp Ile Phe Gly Arg Gln Ser Glu	
216	165 170 175	
217	ATA GAG GAT TTG ATT GAC CGT CTA TTG TCT GAA GGT GCA AGT GGG AAA	2373
218	Ile Glu Asp Leu Ile Asp Arg Leu Leu Ser Glu Gly Ala Ser Gly Lys	
219	180 185 190	
220	AAG CTG ACA GTA GTT CCT ATC GTT GGA ATG GGC GGC CAG GGC AAG ACA	2421
221	Lys Leu Thr Val Val Pro Ile Val Gly Met Gly Gly Gln Gly Lys Thr	
222	195 200 205	
223	ACA CTT GCT AAA GCC GTA TAC AAT GAT GAG AGG GTG AAG AAT CAT TTT	2469
224	Thr Leu Ala Lys Ala Val Tyr Asn Asp Glu Arg Val Lys Asn His Phe	
225	210 215 220	
226	GAT TTG AAA GCG TGG TAT TGC GTT TCT GAA GGA TTT GAT GCT TTG AGA	2517
227	Asp Leu Lys Ala Trp Tyr Cys Val Ser Glu Gly Phe Asp Ala Leu Arg	
228	225 230 235 240	
229	ATA ACA AAA GAA TTA CTC CAA GAA ATT GGC AAA TTT GAC TCG AAG GAT	2565
230	Ile Thr Lys Glu Leu Leu Gln Glu Ile Gly Lys Phe Asp Ser Lys Asp	
231	245 250 255	
232	GTC CAC AAC AAT CTT AAC CAG CTT CAA GTC AAA TTG AAG GAA AGT TTG	2613
233	Val His Asn Asn Leu Asn Gln Leu Gln Val Lys Leu Lys Glu Ser Leu	
234	260 265 270	
235	AAG GGA AAG AAG TTC CTT ATT GTT TTG GAT GAT GTG TGG AAT GAA AAT	2661
236	Lys Gly Lys Lys Phe Leu Ile Val Leu Asp Asp Val Trp Asn Glu Asn	
237	275 280 285	
238	TAC AAC GAG TGG AAT GAC TTG AGA AAT ATT TTT GCA CAA GGA GAT ATA	2709
239	Tyr Asn Glu Trp Asn Asp Leu Arg Asn Ile Phe Ala Gln Gly Asp Ile	
240	290 295 300	
241	GGA AGT AAG ATC ATT GTG ACG ACA CGC AAA GAC AGT GTT GCC TTG ATG	2757
242	Gly Ser Lys Ile Ile Val Thr Thr Arg Lys Asp Ser Val Ala Leu Met	
243	305 310 315 320	
244	ATG GGA AAT GAG CAA ATT CGC ATG GGC AAT TTG TCT ACC GAA GCC TCT	2805
245	Met Gly Asn Glu Gln Ile Arg Met Gly Asn Leu Ser Thr Glu Ala Ser	
246	325 330 335	
247	TGG TCT TTA TTT CAA AGA CAT GCA TTT GAA AAC ATG GAT CCT ATG GGA	2853
248	Trp Ser Leu Phe Gln Arg His Ala Phe Glu Asn Met Asp Pro Met Gly	

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/011,307

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Input Set : N:\EBONY'S\US09011307.raw.txt

Output Set: N:\CRF4\09082003\I011307.raw

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

STATISTICS SUMMARY

PATENT APPLICATION: US/09/011,307

DATE: 09/08/2003

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Input Set : N:\EBONY'S\US09011307.raw.txt

Output Set: N:\CRF4\09082003\I011307.raw

Application Serial Number: US/09/011,307

Alpha or Numeric or Xml: Alpha

Application Class:

Application File Date: 07-01-1988

Art Unit: PCT

Software Application: PatentIN1.0

Total Number of Sequences: 12

Total Nucleotides: 6831

Total Amino Acids: 1266

Number of Errors: 0

Number of Warnings: 0

Number of Corrections: 2

MESSAGE SUMMARY

220 C: 2 (Keyword misspelled or invalid format)